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RAW SEQUENCE LISTING

DATE: 09/18/2002

PATENT APPLICATION: US/10/072,602B

TIME: 15:23:30

Input Set : A:\249 revised sequence 2.txt

Output Set: N:\CRF4\09182002\J072602B.raw

3 <110> APPLICANT: University of Utah Research Foundation
4 Cognetix, Inc.
5 Olivera, Baldomero M.
6 McIntosh, J, Michael
7 Watkins, Maren
8 Garrett, James E.
9 Cruz, Lourdes J.
10 Grilley, Michelle
11 Schoenfeld, Robert M.
12 Walker, Craig
13 Shetty, Reshma
14 Jones, Robert M.
16 <120> TITLE OF INVENTION: Cone Snail Peptides
18 <130> FILE REFERENCE: 2314-249
C--> 20 <140> CURRENT APPLICATION NUMBER: US/10/072,602B
C--> 20 <141> CURRENT FILING DATE: 2002-02-11
20 <150> PRIOR APPLICATION NUMBER: US 60/267,408
21 <151> PRIOR FILING DATE: 2001-02-09
23 <160> NUMBER OF SEQ ID NOS: 638
25 <170> SOFTWARE: PatentIn version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 290
29 <212> TYPE: DNA
30 <213> ORGANISM: Conus ammiralis
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (4)..(231)
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37 atc atg gag aaa ctg ata att ctg ctt ctt gtt gct gct gta ctg atg 48
38 Met Glu Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
39 1 5 10 15
41 tcg acc cag gcc ctg gtt gaa cgt gct gga gaa aac cgc tca aag gag 96
42 Ser Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn Arg Ser Lys Glu
43 20 25 30
45 aac atc aat ttt tta tta aaa aga aag aga gct gct gac agg ggg atg 144
46 Asn Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met
47 35 40 45
49 tgg ggc gat tgc aaa gat ggg tta acg aca tgt ttt gcg ccc tca gag 192
50 Trp Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Pro Ser Glu
51 50 55 60
53 tgt tgt tct gag gat tgt gaa ggg agc tgc acg atg tgg tgatgacctc 241
54 Cys Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp
55 65 70 75

pp 6-10

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}

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57 tgaccacaag ccattctgaca tcaccactct cctcttcaga ggcttcaag      290
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 76
61 <212> TYPE: PRT
62 <213> ORGANISM: Conus ammiralis
64 <400> SEQUENCE: 2
65 Met Glu Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
66 1          5          10          15
68 Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn Arg Ser Lys Glu Asn
69          20          25          30
71 Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp
72          35          40          45
74 Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Pro Ser Glu Cys
75          50          55          60
77 Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp
78 65          70          75
80 <210> SEQ ID NO: 3
81 <211> LENGTH: 31
82 <212> TYPE: PRT
83 <213> ORGANISM: Conus ammiralis
85 <220> FEATURE:
86 <221> NAME/KEY: PEPTIDE
87 <222> LOCATION: (1)..(31)
88 <223> OTHER INFORMATION: Xaa at residues 18, 22 and 25 is Glu or gamma-carboxy-Glu;
89 Xaa at residue 16 is Pro or hydroxy-Pro; Xaa at residues 3
90 and 31 is Trp (D or L) or bromo-Trp (D or L)
92 <400> SEQUENCE: 3
W--> 93 Gly Met Xaa Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Xaa
94 1          5          10          15
W--> 96 Ser Xaa Cys Cys Ser Xaa Asp Cys Xaa Gly Ser Cys Thr Met Xaa
97          20          25          30
99 <210> SEQ ID NO: 4
100 <211> LENGTH: 295
101 <212> TYPE: DNA
102 <213> ORGANISM: Conus ammiralis
104 <220> FEATURE:
105 <221> NAME/KEY: CDS
106 <222> LOCATION: (4)..(246)
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110 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met
111 1          5          10          15
113 tcg acc cag gcc ctg cct caa ggt ggt gga gaa aaa cgc cca agg gag      96
114 Ser Thr Gln Ala Leu Pro Gln Gly Gly Gly Glu Lys Arg Pro Arg Glu
115          20          25          30
117 aat atc aga ttt tta tca aaa aga aag aca aat gct gag cgt tgg agg      144
118 Asn Ile Arg Phe Leu Ser Lys Arg Lys Thr Asn Ala Glu Arg Trp Arg
119          35          40          45
121 gag ggc agt tgc acc tct tgg tta gcg acg tgt acg caa gac cag caa      192

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```

122 Glu Gly Ser Cys Thr Ser Trp Leu Ala Thr Cys Thr Gln Asp Gln Gln
123      50                      55                      60
125 tgc tgt act gat gtt tgt tac aaa agg gac tac tgc gcc ttg tgg gat      240
126 Cys Cys Thr Asp Val Cys Tyr Lys Arg Asp Tyr Cys Ala Leu Trp Asp
127      65                      70                      75
129 gac cgc tgaccacaag ccatctgaca tcaccactct cctgttcaga gtcttcaag      295
130 Asp Arg

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131 80

133 <210> SEQ ID NO: 5

134 <211> LENGTH: 81

135 <212> TYPE: PRT

136 <213> ORGANISM: Conus ammiralis

138 <400> SEQUENCE: 5

139 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser

140 1 5 10 15

142 Thr Gln Ala Leu Pro Gln Gly Gly Gly Glu Lys Arg Pro Arg Glu Asn

143 20 25 30

145 Ile Arg Phe Leu Ser Lys Arg Lys Thr Asn Ala Glu Arg Trp Arg Glu

146 35 40 45

148 Gly Ser Cys Thr Ser Trp Leu Ala Thr Cys Thr Gln Asp Gln Gln Cys

149 50 55 60

151 Cys Thr Asp Val Cys Tyr Lys Arg Asp Tyr Cys Ala Leu Trp Asp Asp

152 65 70 75 80

154 Arg

156 <210> SEQ ID NO: 6

157 <211> LENGTH: 36

158 <212> TYPE: PRT

159 <213> ORGANISM: Conus ammiralis

161 <220> FEATURE:

162 <221> NAME/KEY: PEPTIDE

163 <222> LOCATION: (1)..(36)

164 <223> OTHER INFORMATION: Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at

165 residues 1, 9 and 33 is Trp (D or L) or bromo-Trp

166 (D or L); Xaa at residues 25 and 29 is Tyr, 125I-Tyr,

167 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

169 <400> SEQUENCE: 6

W--> 170 Xaa Arg Xaa Gly Ser Cys Thr Ser Xaa Leu Ala Thr Cys Thr Gln Asp

171 1 5 10 15

dl> 173 Gln Gln Cys Cys Thr Asp Val Cys Xaa Lys Arg Asp Xaa Cys Ala Leu

174 20 25 30

W--> 176 Xaa Asp Asp Arg

177 35

179 <210> SEQ ID NO: 7

180 <211> LENGTH: 275

181 <212> TYPE: DNA

182 <213> ORGANISM: Conus ammiralis

184 <220> FEATURE:

185 <221> NAME/KEY: CDS

186 <222> LOCATION: (4)..(219)

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Input Set : A:\249 revised sequence 2.txt

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188 <400> SEQUENCE: 7
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190 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
191 1 5 10 15
193 tcg acc cag gcc ctg ttt caa gaa aaa cgc aca atg aag aag atc gat      96
194 Ser Thr Gln Ala Leu Phe Gln Glu Lys Arg Thr Met Lys Lys Ile Asp
195 20 25 30
197 ttt tta tca aag gga aag gca gat gct gag aag cag agg aag cgc aat      144
198 Phe Leu Ser Lys Gly Lys Ala Asp Ala Glu Lys Gln Arg Lys Arg Asn
199 35 40 45
201 tgc tcg gat gat tgg cag tat tgt gaa agt ccc agt gac tgc tgt agt      192
202 Cys Ser Asp Asp Trp Gln Tyr Cys Glu Ser Pro Ser Asp Cys Cys Ser
203 50 55 60
205 tgg gat tgt gat gtg gtc tgc tcg gga tgaactctga ccacaagtca      239
206 Trp Asp Cys Asp Val Val Cys Ser Gly
207 65 70
209 tccgacatca ccactctcct gttcagaggc ttcaag      275
211 <210> SEQ ID NO: 8
212 <211> LENGTH: 72
213 <212> TYPE: PRT
214 <213> ORGANISM: Conus ammiralis
216 <400> SEQUENCE: 8
217 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
218 1 5 10 15
220 Thr Gln Ala Leu Phe Gln Glu Lys Arg Thr Met Lys Lys Ile Asp Phe
221 20 25 30
223 Leu Ser Lys Gly Lys Ala Asp Ala Glu Lys Gln Arg Lys Arg Asn Cys
224 35 40 45
226 Ser Asp Asp Trp Gln Tyr Cys Glu Ser Pro Ser Asp Cys Cys Ser Trp
227 50 55 60
229 Asp Cys Asp Val Val Cys Ser Gly
230 65 70
232 <210> SEQ ID NO: 9
233 <211> LENGTH: 25
234 <212> TYPE: PRT
235 <213> ORGANISM: Conus ammiralis
237 <220> FEATURE:
238 <221> NAME/KEY: PEPTIDE
239 <222> LOCATION: (1)..(25)
240 <223> OTHER INFORMATION: Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at
residue 12
241 is Pro or hydroxy-Pro; Xaa at residues 6 and 18 is Trp (D or L)
242 or bromo-Trp (D or L); Xaa at residue 8 is Tyr, 125I-Tyr, mono-
243 iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
245 <400> SEQUENCE: 9
W--> 246 Asn Cys Ser Asp Asp Xaa Gln Xaa Cys Xaa Ser Xaa Ser Asp Cys Cys
247 1 5 10 15
W--> 249 Ser Xaa Asp Cys Asp Val Val Cys Ser
250 20 25
252 <210> SEQ ID NO: 10

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253 <211> LENGTH: 280
254 <212> TYPE: DNA
255 <213> ORGANISM: Conus ammiralis
257 <220> FEATURE:
258 <221> NAME/KEY: CDS
259 <222> LOCATION: (4)..(246)
261 <400> SEQUENCE: 10
262 atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct cta ctg ttg      48
263   Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Leu Leu Leu
264   1          5          10          15
266 tcg atc cag gcg gta aat caa gaa aaa cac caa cgg gca aag atc aac      96
267 Ser Ile Gln Ala Val Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn
268   20          25          30
270 ttg ctt tca aag aga aag cca cct gct gag cgt tgg tgg cgg tgg gga      144
271 Leu Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly
272   35          40          45
274 gga tgc atg gct tgg ttt ggg aaa tgt tcg aag gac tcg gaa tgt tgt      192
275 Gly Cys Met Ala Trp Phe Gly Lys Cys Ser Lys Asp Ser Glu Cys Cys
276   50          55          60
278 tct aat agt tgt gac ata acg cgc tgc gag tta atg cga ttc cca cca      240
279 Ser Asn Ser Cys Asp Ile Thr Arg Cys Glu Leu Met Arg Phe Pro Pro
280   65          70          75
282 gac tgg tgacatcgac actctcctgt tcagagtctt caag      280
283 Asp Trp
284 80
286 <210> SEQ ID NO: 11
287 <211> LENGTH: 81
288 <212> TYPE: PRT
289 <213> ORGANISM: Conus ammiralis
291 <400> SEQUENCE: 11
292 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Leu Leu Leu Ser
293 1          5          10          15
295 Ile Gln Ala Val Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn Leu
296   20          25          30
298 Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly Gly
299   35          40          45
301 Cys Met Ala Trp Phe Gly Lys Cys Ser Lys Asp Ser Glu Cys Cys Ser
302   50          55          60
304 Asn Ser Cys Asp Ile Thr Arg Cys Glu Leu Met Arg Phe Pro Pro Asp
305 65          70          75          80
306 Trp
308 <210> SEQ ID NO: 12
309 <211> LENGTH: 39
310 <212> TYPE: PRT
311 <213> ORGANISM: Conus ammiralis
313 <220> FEATURE:
314 <221> NAME/KEY: PEPTIDE
315 <222> LOCATION: (1)..(39)
316 <223> OTHER INFORMATION: Xaa at residues 19 and 31 is Glu or gamma-carboxy-Glu; Xaa

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 3,16,18,22,25,31
 Seq#:6; Xaa Pos. 1,3,9,25,29,33
 Seq#:9; Xaa Pos. 6,8,10,12,18
 Seq#:12; Xaa Pos. 1,2,4,10,19,31,36,37,39
 Seq#:15; Xaa Pos. 5,8,14,18,19
 Seq#:18; Xaa Pos. 3,5,7,8,14,18
 Seq#:21; Xaa Pos. 4,7,9,13,17,23,27
 Seq#:24; Xaa Pos. 8,13
 Seq#:27; Xaa Pos. 8,13
 Seq#:30; Xaa Pos. 4,5,11
 Seq#:33; Xaa Pos. 4,7,8,11,12,13,14,25,32
 Seq#:36; Xaa Pos. 4,7,8,11,13,14,25,32
 Seq#:39; Xaa Pos. 4,7,8,11,13,14,21,25,29
 Seq#:42; Xaa Pos. 7,8,11,13,14,21,25
 Seq#:45; Xaa Pos. 4,5,7,8
 Seq#:48; Xaa Pos. 5,6,8,9
 Seq#:51; Xaa Pos. 1,2,5,9
 Seq#:54; Xaa Pos. 4,5,7,8
 Seq#:57; Xaa Pos. 1,2,5,6,9
 Seq#:60; Xaa Pos. 2,3,6,15,17,22,23
 Seq#:63; Xaa Pos. 5,10
 Seq#:66; Xaa Pos. 4,7,13,25,31
 Seq#:69; Xaa Pos. 10,23,25,35
 Seq#:72; Xaa Pos. 10,23,25,35
 Seq#:75; Xaa Pos. 23,25,35
 Seq#:78; Xaa Pos. 23,25,35
 Seq#:81; Xaa Pos. 10,23,25,35
 Seq#:84; Xaa Pos. 13,35
 Seq#:87; Xaa Pos. 9,14,26
 Seq#:90; Xaa Pos. 8,13,25
 Seq#:93; Xaa Pos. 2,3,15,19,22,28,31,36
 Seq#:95; Xaa Pos. 11,13,24
 Seq#:96; Xaa Pos. 4,13,16,25
 Seq#:99; Xaa Pos. 5,13,24,25
 Seq#:102; Xaa Pos. 1,5,13,24,25
 Seq#:105; Xaa Pos. 1,5,11,13,24,25
 Seq#:108; Xaa Pos. 6,7,13,21,22,23,27
 Seq#:111; Xaa Pos. 1,12,16
 Seq#:114; Xaa Pos. 10,11,22,23,24,25
 Seq#:115; Xaa Pos. 7
 Seq#:118; Xaa Pos. 3,7,14,29,31,33,37,43,51,55,63,65
 Seq#:119; N Pos. 87,113,128,139,144,165,526,542,586,593,602,612,621,628,639
 Seq#:119; N Pos. 640,709,714,722,723,726,729,738,744,748,752,758
 Seq#:121; Xaa Pos. 2,3,5,11,13,18,21,30,34,35

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Seq#:124; Xaa Pos. 4,16,31,32,33,35,36,37,40,43,52,54,57,59
Seq#:127; Xaa Pos. 2,12,27,28,32,37,40,56,59
Seq#:128; Xaa Pos. 9,15,23,28
Seq#:129; Xaa Pos. 1,6
Seq#:132; Xaa Pos. 12,14,18,22,27,31
Seq#:135; Xaa Pos. 1,3,12,25,27,30
Seq#:138; Xaa Pos. 10,13,16
Seq#:141; Xaa Pos. 4,10,14,17,32
Seq#:142; Xaa Pos. 2,3,6
Seq#:143; Xaa Pos. 2,6
Seq#:144; Xaa Pos. 3,7
Seq#:145; Xaa Pos. 2,6
Seq#:148; Xaa Pos. 10,23,33,34
Seq#:151; Xaa Pos. 3,10,23,33,34
Seq#:154; Xaa Pos. 3,4,9,12,13,27,28,30
Seq#:157; Xaa Pos. 1,15,17,22,23
Seq#:160; Xaa Pos. 1,13,23,31,35
Seq#:163; Xaa Pos. 11
Seq#:166; Xaa Pos. 6,17,20
Seq#:169; Xaa Pos. 10,19,24
Seq#:172; Xaa Pos. 1,4,7,8,11,13,14,25
Seq#:175; Xaa Pos. 4,5,9,23,24,25
Seq#:176; Xaa Pos. 8,12,22
Seq#:179; Xaa Pos. 6,7,13,20,22
Seq#:182; Xaa Pos. 1,7,11,18,20
Seq#:185; Xaa Pos. 6,16,26,29,41
Seq#:188; Xaa Pos. 2,3,7,13,14
Seq#:189; Xaa Pos. 2,3,7,12,14,17
Seq#:192; Xaa Pos. 7,11,14,17
Seq#:193; Xaa Pos. 4
Seq#:196; Xaa Pos. 4,5,8,9,13,15,42,43
Seq#:199; Xaa Pos. 6,9,17,19,25,31,33
Seq#:202; Xaa Pos. 13,17,22,31,46,47
Seq#:205; Xaa Pos. 1,19,23,25,28,37
Seq#:208; Xaa Pos. 4,8,20
Seq#:209; Xaa Pos. 3,4,6
Seq#:210; Xaa Pos. 7
Seq#:213; Xaa Pos. 3
Seq#:216; Xaa Pos. 3,11,19,24,28,36,38,48,54,56,66,74,84
Seq#:217; Xaa Pos. 1,3
Seq#:220; Xaa Pos. 1,29,33
Seq#:223; Xaa Pos. 4,7,16,22,24,26,30,31
Seq#:226; Xaa Pos. 5,8,14,18,19
Seq#:227; Xaa Pos. 3,4,8,11,12,14,16,22,23
Seq#:230; Xaa Pos. 1,6,11
Seq#:233; Xaa Pos. 3,5,12,18,22,23,27
Seq#:236; Xaa Pos. 4,6,8,12
Seq#:239; Xaa Pos. 3,5,6
Seq#:240; Xaa Pos. 4,7,9,13,23

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Seq#:241; Xaa Pos. 8,13
Seq#:244; Xaa Pos. 1,5,7,9,11,13,14,25,36
Seq#:247; Xaa Pos. 1,5,7,11,13,14,29,36
Seq#:250; Xaa Pos. 3,18,22,23,26,34,42
Seq#:253; Xaa Pos. 8,27,28,44
Seq#:256; Xaa Pos. 7,10,13,16
Seq#:259; Xaa Pos. 1,2,3,5,9,16,31
Seq#:262; Xaa Pos. 1,5,6,9,10,13,15,26,33
Seq#:265; Xaa Pos. 6,12,13,20,25,29
Seq#:268; Xaa Pos. 4,10,11,19,22,29
Seq#:271; Xaa Pos. 1,2,3,5,9,16,31
Seq#:274; Xaa Pos. 1,5,6,9,10,13,15,26,33
Seq#:277; Xaa Pos. 9,11,16
Seq#:280; Xaa Pos. 4,8
Seq#:281; N Pos. 110,115,125,127,128,130,132,135
Seq#:281; Xaa Pos. 37,39,42,43,44
Seq#:282; Xaa Pos. 37,39,42,43,44
Seq#:283; Xaa Pos. 4,7,8
Seq#:286; Xaa Pos. 4
Seq#:289; Xaa Pos. 5,7,8
Seq#:292; Xaa Pos. 3,4,5
Seq#:295; Xaa Pos. 5
Seq#:298; Xaa Pos. 3,6,7
Seq#:301; Xaa Pos. 3,4,6,7
Seq#:304; Xaa Pos. 3,4,7
Seq#:307; Xaa Pos. 1,4,9,11
Seq#:310; Xaa Pos. 1,6
Seq#:313; Xaa Pos. 2,3,15,17,22,23,31,32,36
Seq#:316; Xaa Pos. 1,3,6,15,17,22,23,32,35,37
Seq#:319; Xaa Pos. 2,3,15,17,20,22,28,31,37
Seq#:320; N Pos. 256
Seq#:322; Xaa Pos. 2,3,15,17,22,23,31,32,36
Seq#:325; Xaa Pos. 1,3,11,15,22,23,28,31,32,38
Seq#:328; Xaa Pos. 2,3,18,22
Seq#:331; Xaa Pos. 7,12
Seq#:334; Xaa Pos. 11
Seq#:337; Xaa Pos. 6,10
Seq#:338; N Pos. 35
Seq#:340; Xaa Pos. 11
Seq#:341; N Pos. 95
Seq#:343; Xaa Pos. 6,11
Seq#:346; Xaa Pos. 7,12
Seq#:347; Xaa Pos. 6,11
Seq#:350; Xaa Pos. 5,10
Seq#:353; Xaa Pos. 6,11
Seq#:354; N Pos. 251,253,270,311
Seq#:356; Xaa Pos. 7,12
Seq#:359; Xaa Pos. 1,6,11
Seq#:362; Xaa Pos. 1,11

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Seq#:365; Xaa Pos. 11
Seq#:366; N Pos. 292,303
Seq#:368; Xaa Pos. 8,12
Seq#:371; Xaa Pos. 5,10
Seq#:372; Xaa Pos. 2,5,8,17,23,27,32,38,39,41,43,45,58
Seq#:375; Xaa Pos. 4,5,7,9
Seq#:376; N Pos. 2,3,8,10,18,21,22,28,32,35,38,39,44,50,52,66,67,76,77,80
Seq#:376; N Pos. 84,86,88,89,92,96,97,98,99,107,108,111,112,113,114,115,119
Seq#:376; N Pos. 121,126,130,131,135,136,144,153,154,156,159,166,169,172
Seq#:376; N Pos. 173,174,175,181,182,184,185,193,194,195,209,213,214,226
Seq#:376; N Pos. 227,228,230,233,234,235,236,248,250,252,254,257,260,261
Seq#:376; N Pos. 262,266,269,295,303,331,340,345,380,407,439,525,533
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Seq#:378; Xaa Pos. 1,5,11
Seq#:381; Xaa Pos. 1,5
Seq#:384; Xaa Pos. 2,6,10,12
Seq#:387; Xaa Pos. 2,6
Seq#:390; Xaa Pos. 6,10,12
Seq#:393; Xaa Pos. 1,3,8,11,14,16
Seq#:396; Xaa Pos. 1,3,8,11,14,16
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Seq#:402; Xaa Pos. 6,10
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Seq#:404; Xaa Pos. 6,13
Seq#:407; Xaa Pos. 1,7,14
Seq#:410; Xaa Pos. 1,2,7,14,15
Seq#:413; Xaa Pos. 1,2,7,14,15
Seq#:416; Xaa Pos. 5
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Seq#:418; N Pos. 193
Seq#:420; Xaa Pos. 4,6,7,10,13
Seq#:423; Xaa Pos. 6,11,12,13,14
Seq#:424; N Pos. 210
Seq#:426; Xaa Pos. 2,7,8,14,19
Seq#:429; Xaa Pos. 5,10,12
Seq#:432; Xaa Pos. 6,13
Seq#:435; Xaa Pos. 5,6,12
Seq#:438; Xaa Pos. 7,8,14
Seq#:441; Xaa Pos. 6,7,10,13
Seq#:444; Xaa Pos. 6,7,13
Seq#:447; Xaa Pos. 6,7,9,15
Seq#:450; Xaa Pos. 2,7,10,13
Seq#:453; Xaa Pos. 7,15
Seq#:454; N Pos. 8,14,15,22,25,27,32,33,37,52,59,60,65,75,78,87,88,93,101
Seq#:454; N Pos. 104,106,108,110,114,116,120,130,131,132,136,141,146,151
Seq#:454; N Pos. 157,159,172,175,176,183,184,186,189,190,195,198,201,202
Seq#:454; N Pos. 206,209,210,211,213,219,220,224,228,235,242,244,250,255
Seq#:454; N Pos. 258,259,262,269,276,290,294,301,306,308,309,316,318,320

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/18/2002
PATENT APPLICATION: US/10/072,602B TIME: 15:23:31

Input Set : A:\249 revised sequence 2.txt
Output Set: N:\CRF4\09182002\J072602B.raw

Seq#:454; N Pos. 322,324,336,372
Seq#:456; Xaa Pos. 6,7,8,9,11,12,14,15,16
Seq#:465; Xaa Pos. 14,26,31
Seq#:467; Xaa Pos. 9,13,17
Seq#:468; Xaa Pos. 16
Seq#:469; Xaa Pos. 13
Seq#:470; Xaa Pos. 16
Seq#:471; Xaa Pos. 1,5,6,10,15,26,33
Seq#:473; Xaa Pos. 3,7,8,14
Seq#:475; Xaa Pos. 16
Seq#:476; Xaa Pos. 18
Seq#:477; Xaa Pos. 18
Seq#:478; Xaa Pos. 19
Seq#:479; Xaa Pos. 9,13
Seq#:531; Xaa Pos. 12
Seq#:532; Xaa Pos. 11
Seq#:542; Xaa Pos. 3
Seq#:543; Xaa Pos. 5,6
Seq#:548; Xaa Pos. 7,13,21,22,27
Seq#:569; Xaa Pos. 4,13,16
Seq#:585; Xaa Pos. 2,3,12,14
Seq#:622; Xaa Pos. 3
Seq#:625; Xaa Pos. 9
Seq#:627; Xaa Pos. 3
Seq#:628; Xaa Pos. 2